

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	5108	cleaning near4 detergent	USPAT	OR	OFF	2005/05/05 20:14
L2	58	cleaning near4 cellulase	USPAT	OR	OFF	2005/05/05 20:14
L3	36	L1 and L2 and cellulose	USPAT	OR	OFF	2005/05/05 20:14
L4	9	L3 and (cellulose adj binding adj domain)	USPAT	OR	OFF	2005/05/05 20:14
L5	1	L4 and thermostable	USPAT	OR	OFF	2005/05/05 20:14
L6	11	L3 and thermostable	USPAT	OR	OFF	2005/05/05 20:15
L7	1	I6 and cbd	USPAT	OR	OFF	2005/05/05 20:15



PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

Search for

Limits Preview/Index History Clipboard Details

 Features: ☐ SNP ☐ CDD ☒ MGC ☐ HPRD ☐ STS

Item 1 - 7 of 7

☐ 1: [P54583](#). Reports Endoglucanase E1 ...[gi:1708075]

BLink,
Domains,
Links

LOCUS P54583 562 aa linear BCT 01-MAY-

DEFINITION Endoglucanase E1 precursor (Endo-1,4-beta-glucanase E1) (Cellul E1) (Endocellulase E1).

ACCESSION P54583

VERSION P54583 GI:1708075

DBSOURCE swissprot: locus GUN1_ACICE, accession [P54583](#);
class: standard.
created: Oct 1, 1996.
sequence updated: Oct 1, 1996.
annotation updated: May 1, 2005.
xrefs: [U33212.1](#), [AAA75477.1](#), [1C0DA](#), [1C0DB](#), [1ECEA](#), [1ECEB](#)
xrefs (non-sequence databases): InterProIPR001919,
InterProIPR008965, InterProIPR001547, PfamPF00553, PfamPF00150,
SMARTSM00637, PROSITEPS00659

KEYWORDS 3D-structure; Carbohydrate metabolism; Cellulose degradation;
Glycosidase; Hydrolase; Polysaccharide degradation; Signal.

SOURCE Acidothermus cellulolyticus

ORGANISM [Acidothermus cellulolyticus](#)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Frankineae; Acidothermaceae; Acidothermus.

REFERENCE 1 (residues 1 to 562)

AUTHORS Laymon,R.A., Himmel,M.E. and Thomas,S.R.

TITLE Direct Submission

JOURNAL Submitted (??-AUG-1995)

REMARK NUCLEOTIDE SEQUENCE.
STRAIN=ATCC 43068 / 11B

REFERENCE 2 (residues 1 to 562)

AUTHORS Sakon,J., Adney,W.S., Himmel,M.E., Thomas,S.R. and Karplus,P.A.

TITLE Crystal structure of thermostable family 5 endocellulase E1 fro
Acidothermus cellulolyticus in complex with cellotetraose

JOURNAL Biochemistry 35 (33), 10648-10660 (1996)

PUBMED [8718854](#)

REMARK X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 42-398.

COMMENT [FUNCTION] Has a very high specific activity on

carboxymethylcellulose.

[CATALYTIC ACTIVITY] Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucans.

[BIOPHYSICOCHEMICAL PROPERTIES] Temperature dependence: Optimum temperature is 81 degrees Celsius. Thermostable.

[SIMILARITY] Belongs to the glycosyl hydrolase 5 (cellulase A) family.

[SIMILARITY] Contains 1 CBM2 (carbohydrate binding type-2) domain

FEATURES	Location/Qualifiers
source	1..562 /organism="Acidothermus cellulolyticus" /db_xref="taxon:28049"
<u>Protein</u>	1..562 /product="Endoglucanase E1 precursor" /EC_number="3.2.1.4"
<u>Region</u>	1..41 /region_name="Signal" /evidence=experimental
<u>Region</u>	42..562 /region_name="Mature chain" /note="Endoglucanase E1." /evidence=experimental
<u>Region</u>	42..400 /region_name="Domain" /note="Catalytic." /evidence=experimental
<u>Region</u>	48..50 /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	51..52 /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	53..55 /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	57..58 /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	61..62 /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	65..68 /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	72 /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	73 /region_name="Hydrogen bonded turn" /evidence=experimental

<u>Bond</u>	bond(75,161) /bond_type="disulfide" /evidence=experimental
<u>Region</u>	75..76 /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	80..84 /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	87..96 /region_name="Helical region" /evidence=experimental
<u>Region</u>	97..98 /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	101..107 /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	108..111 /region_name="Helical region" /evidence=experimental
<u>Region</u>	113..114 /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	127..129 /region_name="Helical region" /evidence=experimental
<u>Region</u>	130..131 /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	134..147 /region_name="Helical region" /evidence=experimental
<u>Region</u>	148..149 /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	151..158 /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	160 /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	161..162 /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	163 /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	175..188 /region_name="Helical region"

Region /evidence=experimental
189..191
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 193..194
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 195..199
/region_name="Beta-strand region"
/evidence=experimental

Site 203
/site_type="active"
/note="Proton donor."
/evidence=experimental

Region 206..207
/region_name="Hydrogen bonded turn"
/evidence=experimental

Bond bond(209,212)
/bond_type="disulfide"
/evidence=experimental

Region 209
/region_name="Beta-strand region"
/evidence=experimental

Region 215..217
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 218
/region_name="Beta-strand region"
/evidence=experimental

Region 219..230
/region_name="Helical region"
/evidence=experimental

Region 231..233
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 235..236
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 238..242
/region_name="Beta-strand region"
/evidence=experimental

Region 244
/region_name="Beta-strand region"
/evidence=experimental

Region 246..247
/region_name="Beta-strand region"
/evidence=experimental

Region 248..249
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 250..251
/region_name="Beta-strand region"
/evidence=experimental

Region 254..255
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 257
/region_name="Beta-strand region"
/evidence=experimental

Region 259..263
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 274..279
/region_name="Beta-strand region"
/evidence=experimental

Region 283..285
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 289..292
/region_name="Helical region"
/evidence=experimental

Region 294..299
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 300..307
/region_name="Helical region"
/evidence=experimental

Region 308
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 309..313
/region_name="Helical region"
/evidence=experimental

Region 314..315
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 319..323
/region_name="Beta-strand region"
/evidence=experimental

Site 323
/site_type="active"
/note="Nucleophile."
/evidence=experimental

Region 331..343
/region_name="Helical region"
/evidence=experimental

Region 344
/region_name="Hydrogen bonded turn"
/evidence=experimental

Region 347..350

```

/region_name="Helical region"
/evidence=experimental
Region 351..352
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 356..359
/region_name="Beta-strand region"
/evidence=experimental
Region 367..369
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 373
/region_name="Beta-strand region"
/evidence=experimental
Region 375..376
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 380
/region_name="Beta-strand region"
/evidence=experimental
Region 382..387
/region_name="Helical region"
/evidence=experimental
Region 388
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 389..391
/region_name="Helical region"
/evidence=experimental
Region 401..461
/region_name="Domain"
/note="Pro/Ser/Thr-rich (linker)."
/evidence=experimental
Region 462..562
/region_name="Domain"
/note="CBM2."
/evidence=experimental

```

ORIGIN

```

1 mpralrrvpqg srvmrlrvgvv vavlalvaal anlavprpar aaggggywhts greildannv
61 pvriaginwf gfetcnyvvh glwsrdyrsm ldqikslgyn tirlpysddi lkpgtmpnsi
121 nfyqmnqdlq gltslqvmdk ivayaggigl riildrhrpd csgqsalwyt ssvseatwis
181 dlqalaaqyk gnptvvgfdl hnephdpacw gcgdpsidwr laaeragnav lsvnpnllif
241 vegvqsyngd sywwggnlqg agqypvvlv pnrlvysahd yatsvypqtw fsdptfpnm
301 pgiwnknwgy lfnqniapvw lgefgttlqs ttdqtwlktl vqylrptaay gadsfqwtfw
361 swnpdsgdtg gilkdwdqtv dtvkdgylap ikssifdpvg asaspspsps psvspspsp
421 psasrtptpt ptptasptpt ltptatptpt asptpsptaa sgarctasyq vnsdwgngft
481 vtvavtnsgs vatktwtvsw tfggngtitn swnaavtqng qsvtarnmsy nnviqpgqnt
541 tfgfqasytg snaaptvaca as

```

//

□2: CAD42489. Reports unnamed protein p...[gi:21900783]

[BLink](#), [Links](#)

LOCUS CAD42489 562 aa linear BCT 16-JUL-
 DEFINITION unnamed protein product [Acidothermus cellulolyticus].
 ACCESSION CAD42489
 VERSION CAD42489.1 GI:21900783
 DBSOURCE embl accession AX467594.1
 KEYWORDS .
 SOURCE Acidothermus cellulolyticus
 ORGANISM Acidothermus cellulolyticus
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Frankineae; Acidothermaceae; Acidothermus.
 REFERENCE 1
 AUTHORS Sticklen,M.B., Dale,B.E. and Maqbool,S.
 TITLE Transgenic plants containing ligninase and cellulase which degr
 lignin and cellulose to fermentable sugars
 JOURNAL Patent: WO 0234926-A 02-MAY-2002;
 MICHIGAN STATE UNIVERSITY (US)
 FEATURES Location/Qualifiers
 source 1..562
 /organism="Acidothermus cellulolyticus"
 /db_xref="taxon:28049"
 Protein 1..562
 /name="unnamed protein product"
 CDS 1..562
 /coded_by="AX467594.1:824..2512"
 /note="E I beta-1,4-endoglucanase precursor"
 /transl_table=11

ORIGIN

```

1 mpralrrvpq srvmrlrvgvv vavlalvaal anlavprpar aaggggywhts greildannv
61 pvriaginwf gfetcnyvvh glwsrdyrsm ldqikslgyn tirlpysddi lkpgtmpnsi
121 nfyqmnqdlq gltslqvmdk ivayagqigl riildrhrpd csgqsalwyt ssvseatwis
181 dlqalaraqyk gnptvvgfdl hnephdpacw gcgdpdswr laaeragnav lsvnpnllif
241 vegvqsyngd sywwggnlqg agqypvvlv pnrlyvsahd yatsvypqtw fsdptfpnm
301 pgiwnknwgy lfnqniapvw lgefgttlqs ttdqtwlktl vqylrptaay gadsfqwtfw
361 swnpdsgdtg gilkdwdqtv dtvkdgylap ikssifdpvg asaspssqps psvspspsp
421 psasrtptpt ptptasptpt ltptatptpt asptpsptaa sgarctasyq vnsdwngnft
481 vtvavtnsgs vatktwtvsw tfggngtitn swnaavtqng qsvtarnmsy nnviqpgqnt
541 tfgfqasytg snaaptvaca as

```

//

□3: 1C0DB. Reports Chain B, Endocell...[gi:5821930]

[BLink](#),
[Domains](#),
[Links](#)

LOCUS 1C0D_B 358 aa linear BCT 15-JUL-
 DEFINITION Chain B, Endocellulase E1 From Acidothermus Cellulolyticus Muta
 Y245g.
 ACCESSION 1C0D_B

VERSION 1COD_B GI:5821930
DBSOURCE pdb: molecule 1COD, chain 66, release Jul 15, 1999;
deposition: Jul 15, 1999;
class: Hydrolase;
source: Mol_id: 1; Organism_scientific: Acidothermus
Cellulolyticus; Organism_common: Thermophilic Bacterium From Th
Yellowstone National Park; Expression_system: Escherichia Coli;
Expression_system_common: Bacteria;
Exp. method: X-Ray Diffraction.

KEYWORDS .

SOURCE Acidothermus cellulolyticus
ORGANISM Acidothermus cellulolyticus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Frankineae; Acidothermaceae; Acidothermus.

REFERENCE 1 (residues 1 to 358)
AUTHORS Mccarley,J.R., Lovett,R.M., Sakon,J., Himmel,M.E. and Baker,J.O
TITLE Catalytically Enhanced Endocellulase E1 From Acidothermus
Cellulolyticus
JOURNAL Unpublished

REFERENCE 2 (residues 1 to 358)
AUTHORS Mccarley,J.R., Lovett,R.M., Sakon,J., Himmel,M.E. and Baker,J.O
TITLE Direct Submission
JOURNAL Submitted (15-JUL-1999)

COMMENT Revision History:
JUL 23 99 Initial Entry.

FEATURES Location/Qualifiers
source 1..358
/organism="Acidothermus cellulolyticus"
/db_xref="taxon:28049"
SecStr 5..10
/sec_str_type="sheet"
/note="strand 16"
SecStr 11..16
/sec_str_type="sheet"
/note="strand 17"
SecStr 23..29
/sec_str_type="sheet"
/note="strand 18"
Bond bond(34,120)
/bond_type="disulfide"
SecStr 46..56
/sec_str_type="helix"
/note="helix 7"
SecStr 59..65
/sec_str_type="sheet"
/note="strand 19"
SecStr 93..106
/sec_str_type="helix"
/note="helix 8"
SecStr 107..115

SecStr /sec_str_type="sheet"
/note="strand 20"
134..148
/sec_str_type="helix"
/note="helix 9"
SecStr 155..159
/sec_str_type="sheet"
/note="strand 21"
SecStr 167..170
/sec_str_type="sheet"
/note="strand 22"
Bond bond(168,171)
/bond_type="disulfide"
SecStr 176..179
/sec_str_type="sheet"
/note="strand 23"
SecStr 180..192
/sec_str_type="helix"
/note="helix 10"
SecStr 196..202
/sec_str_type="sheet"
/note="strand 24"
SecStr 204..207
/sec_str_type="sheet"
/note="strand 25"
SecStr 208..211
/sec_str_type="sheet"
/note="strand 26"
SecStr 232..240
/sec_str_type="sheet"
/note="strand 27"
SecStr 259..266
/sec_str_type="helix"
/note="helix 11"
SecStr 277..284
/sec_str_type="sheet"
/note="strand 28"
SecStr 290..302
/sec_str_type="helix"
/note="helix 12"
SecStr 314..319
/sec_str_type="sheet"
/note="strand 29"
SecStr 355..358
/sec_str_type="sheet"
/note="strand 30"

ORIGIN

1 aggywhtsg reildannvp vriaginwfg fetchnyvvhg lwsrdyrsml dqikslgynt
61 irlpysddil kpgtmpnsin fyqmnqdlqg ltslqvmdki vayaggiglr iildrhrpdc
121 sgqsalwyts svseatwisd lqalaqrykg nptvvgfdlh nephdpacwg cgdpsidwrl

```

181 aaeragnavl svnpnllifv egvqsyngds ywwggnlqga gqypvvlnvp nrlvysahdy
241 atsvgpqtwf sdptfpnmp giwnknwgyf fnqniapvwl gefgttlqst tdqtwlktlv
301 qylrptaqyg adsfqwtfws wnpdsgdtgg ilkddwqtvd tdkdgylapi kssifdpv

```

//

BLink,
Domains,
Links
4: 1C0DA Reports Chain A, Endocell...[gi:5821929]

LOCUS 1C0D_A 358 aa linear BCT 15-JUL-
 DEFINITION Chain A, Endocellulase E1 From Acidothermus Cellulolyticus Muta
 Y245g.
 ACCESSION 1C0D_A
 VERSION 1C0D_A GI:5821929
 DBSOURCE pdb: molecule 1C0D, chain 65, release Jul 15, 1999;
 deposition: Jul 15, 1999;
 class: Hydrolase;
 source: Mol_id: 1; Organism_scientific: Acidothermus
 Cellulolyticus; Organism_common: Thermophilic Bacterium From Th
 Yellowstone National Park; Expression_system: Escherichia Coli;
 Expression_system_common: Bacteria;
 Exp. method: X-Ray Diffraction.

KEYWORDS .
 SOURCE Acidothermus cellulolyticus
 ORGANISM Acidothermus cellulolyticus
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Frankineae; Acidothermaceae; Acidothermus.

REFERENCE 1 (residues 1 to 358)
 AUTHORS Mccarley, J.R., Lovett, R.M., Sakon, J., Himmel, M.E. and Baker, J.O
 TITLE Catalytically Enhanced Endocellulase E1 From Acidothermus
 Cellulolyticus
 JOURNAL Unpublished

REFERENCE 2 (residues 1 to 358)
 AUTHORS Mccarley, J.R., Lovett, R.M., Sakon, J., Himmel, M.E. and Baker, J.O
 TITLE Direct Submission
 JOURNAL Submitted (15-JUL-1999)

COMMENT Revision History:
 JUL 23 99 Initial Entry.

FEATURES Location/Qualifiers
 source 1..358
 /organism="Acidothermus cellulolyticus"
 /db_xref="taxon:28049"
SecStr 5..10
 /sec_str_type="sheet"
 /note="strand 1"
SecStr 11..16
 /sec_str_type="sheet"
 /note="strand 2"
SecStr 23..29

	/sec_str_type="sheet"
	/note="strand 3"
<u>Bond</u>	bond(34,120)
	/bond_type="disulfide"
<u>SecStr</u>	46..56
	/sec_str_type="helix"
	/note="helix 1"
<u>SecStr</u>	59..65
	/sec_str_type="sheet"
	/note="strand 4"
<u>SecStr</u>	93..106
	/sec_str_type="helix"
	/note="helix 2"
<u>SecStr</u>	107..115
	/sec_str_type="sheet"
	/note="strand 5"
<u>SecStr</u>	134..148
	/sec_str_type="helix"
	/note="helix 3"
<u>SecStr</u>	155..159
	/sec_str_type="sheet"
	/note="strand 6"
<u>SecStr</u>	167..170
	/sec_str_type="sheet"
	/note="strand 7"
<u>Bond</u>	bond(168,171)
	/bond_type="disulfide"
<u>SecStr</u>	176..179
	/sec_str_type="sheet"
	/note="strand 8"
<u>SecStr</u>	180..192
	/sec_str_type="helix"
	/note="helix 4"
<u>SecStr</u>	196..202
	/sec_str_type="sheet"
	/note="strand 9"
<u>SecStr</u>	204..207
	/sec_str_type="sheet"
	/note="strand 10"
<u>SecStr</u>	208..211
	/sec_str_type="sheet"
	/note="strand 11"
<u>SecStr</u>	232..240
	/sec_str_type="sheet"
	/note="strand 12"
<u>SecStr</u>	259..266
	/sec_str_type="helix"
	/note="helix 5"
<u>SecStr</u>	277..284
	/sec_str_type="sheet"

```

          /note="strand 13"
SecStr    290..302
          /sec_str_type="helix"
          /note="helix 6"
SecStr    314..319
          /sec_str_type="sheet"
          /note="strand 14"
SecStr    355..358
          /sec_str_type="sheet"
          /note="strand 15"

```

ORIGIN

```

      1 agggwyhtsg reildannvp vriaginwfg fetcnvvhg lwsrdyrsml dqikslgynt
     61 irlpysddil kpgtmpnsin fyqmnqdlqg ltslqvmcki vayagqiglr iildrhrpdc
    121 sgqsalwyts svseatwisd lqalaqrykg nptvvgfdlh nephdpacwg cgdpsidwrl
    181 aaeragnavl svnpnllifv egvqsyngds ywwggnlqga gqypvvlnvp nrlvysahdy
    241 atsvgpqtwf sdptfpnmp giwnknwgyl fnqniapvwl gefgttlqst tdqtwlktlv
    301 qylrptaqyg adsfqwtfws wnpdsgdtgg ilkddwqtvd tdkdgylapi kssifdpv

```

//

5: 1ECEB. Reports Chain B, Acidothe...[gi:1827682]

BLink,
Domains,
Links

LOCUS 1ECE_B 358 aa linear BCT 04-APR-
 DEFINITION Chain B, Acidothermus Cellulolyticus Endocellulase E1 Catalytic
 Domain In Complex With A Cellotetraose.
 ACCESSION 1ECE_B
 VERSION 1ECE_B GI:1827682
 DBSOURCE pdb: molecule 1ECE, chain 66, release Apr 4, 1996;
 deposition: Apr 4, 1996;
 class: Glycosyl Hydrolase;
 source: Mol_id: 1; Organism_scientific: Acidothermus
 Cellulolyticus; Expression_system: Streptomyces Lividans;
 Expression_system_strain: Tk24; Expression_system_plasmid: Pij7
 Expression_system_gene: Pvu I Fragment Of A. Cellulolyticus Gen
 Dna Carrying Native E1 Gene;
 Exp. method: X-Ray Diffraction.

KEYWORDS .

SOURCE Acidothermus cellulolyticus
 ORGANISM Acidothermus cellulolyticus
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 Frankineae; Acidothermaceae; Acidothermus.

REFERENCE 1 (residues 1 to 358)
 AUTHORS Sakon,J., Thomas,S.R., Himmel,M.E. and Karplus,P.A.
 TITLE Direct Submission
 JOURNAL Submitted (04-APR-1996)

COMMENT Revision History:
 OCT 14 96 Initial Entry.

FEATURES Location/Qualifiers

source 1..358
/organism="Acidothermus cellulolyticus"
/db_xref="taxon:28049"

SecStr 5..10
/sec_str_type="sheet"
/note="strand 15"

SecStr 11..16
/sec_str_type="sheet"
/note="strand 16"

SecStr 23..29
/sec_str_type="sheet"
/note="strand 17"

Bond bond(34,120)
/bond_type="disulfide"

SecStr 46..56
/sec_str_type="helix"
/note="helix 7"

SecStr 59..65
/sec_str_type="sheet"
/note="strand 18"

SecStr 93..107
/sec_str_type="helix"
/note="helix 8"

SecStr 109..115
/sec_str_type="sheet"
/note="strand 19"

SecStr 134..148
/sec_str_type="helix"
/note="helix 9"

SecStr 155..159
/sec_str_type="sheet"
/note="strand 20"

SecStr 167..170
/sec_str_type="sheet"
/note="strand 21"

Bond bond(168,171)
/bond_type="disulfide"

SecStr 176..179
/sec_str_type="sheet"
/note="strand 22"

SecStr 180..192
/sec_str_type="helix"
/note="helix 10"

SecStr 196..202
/sec_str_type="sheet"
/note="strand 23"

SecStr 204..207
/sec_str_type="sheet"
/note="strand 24"

SecStr 208..211

```

                /sec_str_type="sheet"
                /note="strand 25"
SecStr          232..238
                /sec_str_type="sheet"
                /note="strand 26"
SecStr          259..266
                /sec_str_type="helix"
                /note="helix 11"
SecStr          277..282
                /sec_str_type="sheet"
                /note="strand 27"
SecStr          290..302
                /sec_str_type="helix"
                /note="helix 12"
SecStr          314..319
                /sec_str_type="sheet"
                /note="strand 28"

```

ORIGIN

```

    1 agggwyhtsg reildannvp vriaginwfg fetcnvvhg lwsrdyrsml dqikslgynt
   61 irlpysddil kpgtmpnsin fyqmnqdlqg ltslqvmdki vayagqiglr iildrhrpdc
  121 sgqsalwyts svseatwisd lqalaqrykg nptvvgfdlh nephdpacwg cgdpsidwrl
  181 aaeragnavl svnpnllifv egvqsyngds ywwggnlqga gqypvvlnvp nrlvysahdy
  241 atsvypqtwf sdptfpnmp giwnknwgyl fnqniapvwl gefgttlqst tdqtwlktlv
  301 qylrptaqyg adsfqwtfws wnpdsgdtgg ilkddwqtv d tvkdgylapi kssifdpv

```

//

6: 1ECEA. Reports Chain A, Acidothe...[gi:1827681]

[BLink](#),
[Domains](#),
[Links](#)

LOCUS 1ECE_A 358 aa linear BCT 04-APR-
DEFINITION Chain A, Acidothermus Cellulolyticus Endocellulase E1 Catalytic
Domain In Complex With A Cellotetraose.
ACCESSION 1ECE_A
VERSION 1ECE_A GI:1827681
DBSOURCE pdb: molecule 1ECE, chain 65, release Apr 4, 1996;
deposition: Apr 4, 1996;
class: Glycosyl Hydrolase;
source: Mol_id: 1; Organism_scientific: Acidothermus
Cellulolyticus; Expression_system: Streptomyces Lividans;
Expression_system_strain: Tk24; Expression_system_plasmid: Pij7
Expression_system_gene: Pvu I Fragment Of A. Cellulolyticus Gen
Dna Carrying Native E1 Gene;
Exp. method: X-Ray Diffraction.
KEYWORDS .
SOURCE Acidothermus cellulolyticus
ORGANISM Acidothermus cellulolyticus
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Frankineae; Acidothermaceae; Acidothermus.

REFERENCE 1 (residues 1 to 358)
AUTHORS Sakon,J., Thomas,S.R., Himmel,M.E. and Karplus,P.A.
TITLE Direct Submission
JOURNAL Submitted (04-APR-1996)
COMMENT Revision History:
OCT 14 96 Initial Entry.

FEATURES Location/Qualifiers
source 1..358
/organism="Acidothermus cellulolyticus"
/db_xref="taxon:28049"
SecStr 5..10
/sec_str_type="sheet"
/note="strand 1"
SecStr 11..16
/sec_str_type="sheet"
/note="strand 2"
SecStr 23..29
/sec_str_type="sheet"
/note="strand 3"
Bond bond(34,120)
/bond_type="disulfide"
SecStr 46..56
/sec_str_type="helix"
/note="helix 1"
SecStr 59..65
/sec_str_type="sheet"
/note="strand 4"
SecStr 93..107
/sec_str_type="helix"
/note="helix 2"
SecStr 109..115
/sec_str_type="sheet"
/note="strand 5"
SecStr 134..148
/sec_str_type="helix"
/note="helix 3"
SecStr 155..159
/sec_str_type="sheet"
/note="strand 6"
SecStr 167..170
/sec_str_type="sheet"
/note="strand 7"
Bond bond(168,171)
/bond_type="disulfide"
SecStr 176..179
/sec_str_type="sheet"
/note="strand 8"
SecStr 180..192
/sec_str_type="helix"
/note="helix 4"

SecStr 196..202
/sec_str_type="sheet"
/note="strand 9"

SecStr 204..207
/sec_str_type="sheet"
/note="strand 10"

SecStr 208..211
/sec_str_type="sheet"
/note="strand 11"

SecStr 232..238
/sec_str_type="sheet"
/note="strand 12"

SecStr 259..266
/sec_str_type="helix"
/note="helix 5"

SecStr 277..282
/sec_str_type="sheet"
/note="strand 13"

SecStr 290..302
/sec_str_type="helix"
/note="helix 6"

SecStr 314..319
/sec_str_type="sheet"
/note="strand 14"

ORIGIN

```

1  agggwyhtsg reildannvp vriaginwfg fetcnyvvhg lwsrdyrsml dqikslgynt
61  irlpysddil kpgtmpnsin fyqmnqdlqg ltslqvmdki vayagqiglr iildrhrpdc
121 sgqsalwyts svseatwisd lqalaqrykg nptvvgfdlh nephdpacwg cgdpsidwrl
181 aaeragnavl svnpnllifv egvqsyngds ywwggnlqga gqypvvlnvp nrlvysahdy
241 atsvypqtwf sdptfpnmp giwnknwgyf fnqniapvwl gefgttlqst tdqtwlktlv
301 qylrptaqyg adsfqwtfws wnpdsgdtgg ilkddwqtvd tvkdgylapi kssifdpv

```

//

7: [AAA75477](#). Reports E I beta-1,4-endo...[gi:988300]

BLink,
Domains,
Links

LOCUS AAA75477 562 aa linear BCT 19-SEP-

DEFINITION E I beta-1,4-endoglucanase precursor.

ACCESSION AAA75477

VERSION AAA75477.1 GI:988300

DBSOURCE locus ACU33212 accession [U33212.1](#)

KEYWORDS .

SOURCE Acidothermus cellulolyticus

ORGANISM [Acidothermus cellulolyticus](#)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Frankineae; Acidothermaceae; Acidothermus.

REFERENCE 1 (residues 1 to 562)

AUTHORS Laymon, R.A., Himmel, M.E. and Thomas, S.R.

TITLE Direct Submission
JOURNAL Submitted (04-AUG-1995) Steven R. Thomas, Applied Biological Sciences, National Renewable Energy Laboratory, 1617 Cole Blvd. Golden, CO 80401, USA
COMMENT Method: conceptual translation.
FEATURES Location/Qualifiers
 source 1..562
 /organism="Acidothermus cellulolyticus"
 /strain="11B (ATCC 43068)"
 /db_xref="taxon:28049"
 Protein 1..562
 /product="E I beta-1,4-endoglucanase precursor"
 sig_peptide 1..41
 mat_peptide 42..562
 /product="E I beta-1,4-endoglucanase"
 /EC_number="3.2.1.4"
 /note="cellulase"
 CDS 1..562
 /coded_by="U33212.1:824..2512"
 /transl_table=11

ORIGIN

```
1 mpralrrvpg srvmlrvgvv vavlalvaal anlavprpar aagggywhs greildannv
61 pvriaginwf gfetchnyvvh glwsrdyism ldqikslgyn tirlpysddi lkpgtmpnsi
121 nfyqmnqdlq gltslqvmdk ivayagqigl riildrhrpd csgqsalywt ssvseatwis
181 dlqalaqryk gnptvvgfdl hnephdpacw gcgdpsidwr laaeragnav lsvnpnllif
241 vegvqsyngd sywwggnlqg agqypvvlv pnrlvysahd yatsvypqtw fsdptfpnnm
301 pgiwnknwgy lfnqniapvw lgefgttlqs ttdqtwlktl vqylrptaay gadsfqwtfw
361 swnpdsgdtg gilkdwdqtv dtvkdgylap ikssifdpvg asaspssqps psvspspsp
421 psasrtptpt ptptasptpt ltptatptpt asptpsptaa sgactasyq vnsdwgngft
481 vtvavtnsgs vatktwtvsw tfggngtitn swnaavtqng qsvtarnmsy nnviqpgqnt
541 tfgfqasytg snaaptvaca as
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10